

ABSTRACT

A method of handling a database for bioinformatics is disclosed. A server receives a sequence to be compared and analyzed from the user terminal to store it in a queue. When there exist other sequences to be compared and analyzed, the server reads the sequence of the current
5 order from the database to compare it with all of sequences stored in the queue. That is, the server accesses the database once to use it for all of user requests currently being processed. Because the server accesses the database only once for each user request, the average system cost and response time are decreased. Furthermore, the threshold of the user request arrival rate that can be received on the same hardware in the present invention is higher compared to the convention
10 method, so that larger amount of users can be provided the comparison/analysis service.